

FILE COPY

GanCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: October 13, 1999, 14:43:47 : Search time 2579.19 Seconds
(without alignments)
Scoring table: IDENTIT_NUC

Scored: 679419 seeds, 1590154680 residues
Perfect score: 9721
Sequence: lagaagaqaaqagagaaaa.....ccgttggactgcaggctcgac 9721
11986.627 Million cell updates/sec

base : GenEmbl: *
1: gb_bai1: *.
2: gb_bar2: *.
3: gb_om: *.
4: gb_ov: *.
5: gb_pat: *.
6: gb_phi: *.
7: gb_p11: *.
8: gb_p12: *.
9: gb_pri1: *.
10: gb_pr2: *.
11: gb_p3: *.
12: gb_rco: *.
13: gb_st: *.
14: gb_ses: *.
15: gb_sy: *.
16: gb_uni: *.
17: gb_vri: *.
18: em_fan: *.
19: em_hsq: *.
20: em_hum1: *.
21: em_hum2: *.
22: em_in: *.
23: em_lor: *.
24: em_lox: *.
25: em_ox: *.
26: em_pat: *.
27: em_ph: *.
28: em_pl: *.
29: em_rro: *.
30: em_stc: *.
31: em_sy: *.
32: em_un: *.
33: em_v1: *.
34: gb_hg1: *.
35: gb_htc2: *.
36: gb_in1: *.
37: gb_in2: *.
38: em_bai1: *.
39: em_bai2: *.
40: em_hum3: *.
41: em_hum4: *.
42: gb_pra: *

2: 7208.8 74.2 7824 9 HUMILB
3: 1688.2 17.4 1773 5 A01613
4: 1107.4 11.4 8760 4 SSPIN1B
5: 807.6 8.3 1473 10 HSPR01B
6: 807.4 8.3 1497 5 E05734
7: 807.4 8.3 1497 9 HUMILBA
8: 788.6 8.1 1507 5 E00846
9: 788.6 8.1 1507 5 E07942
10: 780.8 8.0 1496 9 HUMILB
11: 769.8 7.9 1514 5 I00729
12: 766.6 7.9 1496 9 HUMILIC
13: 764.8 7.9 1404 5 A21148
14: 764.8 7.9 1404 5 E01230
15: 764.8 7.9 1404 26 E11934
16: 764.8 7.9 1404 26 E12090
17: 764.4 7.9 1404 5 I00228
18: 756.4 7.8 1469 5 I01156
19: 637.2 6.6 10156 5 E02498
20: 612.4 6.3 614 14 G10509
21: 573.2 5.9 7100 12 MMILBG
22: 553 5.7 553 10 HSPR01B
23: 457.6 4.7 1124 10 HSILIBR
24: 445.6 4.6 1125 5 E00619
25: 423.2 4.4 775 5 SYNLBA
26: 400 4.1 400 14 G13631
27: 395 4.1 395 10 HSPR01N
28: 379.6 3.9 1473 3 ECU92481
29: 360 3.7 1458 3 PIGPIKRN
30: 331.4 3.4 594 5 E01445
31: 331.2 3.4 1429 5 E01445
32: 325.8 3.4 1895 3 AF026543
33: 307.4 3.2 986 5 E01591
34: 293.4 3.0 1736 3 BOVILB
35: 293.4 3.0 1750 5 I03510
36: 260.6 2.7 502 11 AF043335
C: 37 251.2 2.6 141851 9 HS37N13
38: 250.2 2.6 43748 10 HSB94
39: 250.2 2.6 136298 34 HS796117
C: 40 249.4 2.6 133090 45 AC005474
C: 41 249.4 2.6 162356 42 AC00017
C: 42 249.2 2.6 131070 11 AC005295
C: 43 24.8 2.6 149554 10 AC000111
C: 44 24.8 2.6 1437 12 AF119622
2.5 130988 9 HS364122

ALIGNMENTS

RESULT	1
HSILB	HSILB
LOCUS	HSILB
DEFINITION	Human gene for prointerleukin 1 beta.
ACCESSION	X04500
NID	933788
VERSION	X04500.1
KEYWORDS	GR:33788 interleukin 1 beta.
SOURCE	human.
ORGANISM	Homo sapiens
	Eutheria; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 9721)
AUTHORS	Clark,B.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auton,P.E.
TITLE	Genomic sequence for human prointerleukin 1 beta: Possible evolution from a reverse transcribed prointerleukin 1 alpha gene
JOURNAL	Nucleic Acids Res. 14 (20), 7897-7914 (1986)
MEDLINE	87040762
REMARK	Erratum:[published erratum appears in Nucleic Acids Res 1987 Jan 26;15(2):868]
COMMENT	Data kindly reviewed (13-MAY-1988) by Clark B.D.
FEATURES	LocationQualifiers
Source	1. "9721 /organism="Homo sapiens"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	9717.4	100.0	9721	10 HSILB
				x04500 Human gene

